

U.S. Application Serial No. 10/601,324  
Restriction Requirement mailed December 15, 2005  
Response to Restriction Requirement dated January 31, 2006

Docket No. EPHA2-5001-C1

### AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

#### Listing Of Claims

1 (original). A composition comprising a protein in crystalline form wherein the protein has at least 90% identity with residues 605-883 of SEQ. ID No. 1.

2 (original). A composition according to claim 1 wherein the protein has at least 95% identity with residues 605-883 of SEQ. ID No. 1.

3 (original). A composition according to claim 1 wherein at least a portion of the protein comprises consecutively residues 605-883 of SEQ. ID No. 1.

4 (original). A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5 (original). A composition according to claim 1 wherein the protein crystal has a crystal lattice in a P<sub>3</sub>2<sub>1</sub> space group.

6 (original). A composition according to claim 1 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=72.12Å, b= 72.12Å and c=241.62Å.

7 (original). A composition comprising EPHA2 in crystalline form wherein the crystal has a crystal lattice in a P<sub>3</sub>2<sub>1</sub> space group.

8 (original). A composition comprising EPHA2 in crystalline form wherein the crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=72.12Å, b= 72.12Å and c=241.62Å.

9 (original). A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising: a precipitant solution and a protein wherein the protein has at least 90% identity with residues 605-883 of SEQ. ID No. 1; and

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storing the crystallization volume under conditions suitable for crystal formation of the protein.

10 (original). A method according to claim 9 wherein the protein has at least 95% identity with residues 605-883 of SEQ. ID No. 1.

11 (original). A method according to claim 9 wherein at least a portion of the protein comprises consecutively residues 605-883 of SEQ. ID No. 1.

12 (original). A method according to claim 9 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

13 (original). A method according to claim 9 wherein the protein crystal has a crystal lattice in a P3<sub>2</sub>21 space group.

14 (original). A method according to claim 9 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of a=72.12Å, b= 72.12Å and c=241.62Å.

15 (original). A method according to claim 9, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

16 (original). A composition comprising at least a portion of a protein expressed as SEQ. ID No. 2.

17 (original). A composition comprising an isolated protein consisting of SEQ. ID No. 3.

18 (withdrawn). A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that has at least 90% identity with SEQ. ID No. 3; and

performing rational drug design using a three dimensional structure that is based on the

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obtained structure coordinates.

19 (withdrawn). A method according to claim 18 wherein the protein has at least 95% identity with SEQ. ID No. 3.

20 (withdrawn). A method according to claim 18 wherein the protein crystal has a crystal lattice having unit cell dimensions, +/- 5%, of  $a=72.12\text{\AA}$ ,  $b=72.12\text{\AA}$  and  $c=241.62\text{\AA}$ .

21 (withdrawn). A method according to claim 18 wherein the protein crystal has a crystal lattice in a  $P3_221$  space group.

22 (withdrawn). A method according to claim 18, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

23 (withdrawn). A method according to claim 18, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

24 (withdrawn). A method according to claim 18, the method further comprising comparing activity of the protein in a presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending whether a particular entity is present.

25 (withdrawn). A method according to claim 18, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.